

1 |-----A-----|-----  
TCAAATTTT CTCCAGTTCT AAATATCCGG AAACCTCTTG GGATGCCATT

51 |-----B-----|-----C-----|-----D-----  
GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT

101 |-----E-----|-----F-----|  
CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC

151 |-----G-----|-----H-----|-----  
TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG

201 --F--|-----G-----|-----I-----  
TGGAGTAAGA AGACGTTCTGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT

251 ----|-----J-----|-----K-----|-----L-----  
AGTATCTCCA TTGACGTAAG GGATGAACA CAATCCAACAT ATCCATCGCA

301 -----|-----M-----|-----L-----|-----N-----  
AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTCGAG TGGCCACGCT

351 |  
G [SEQ ID NO:1]

FIGURE 1

1 TCAAATTTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT  
51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT  
101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC  
151 TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG  
201 TGGAGTAAGA AGACGTTTCGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT  
251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAAC TCCATCGCA  
301 AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTGAG TGGCCACGCT  
351 G [SEQ ID NO:2]

FIGURE 2

1     TCAAATTTTT   CTCCAGTTCT   AAATATCCGG   AAACCTCTTG   GGATGCCATT  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      TGAGACTTTT   CAACAAAGGG   TAATATCGGG   AAACCTCCTC   GGATTCCATT

51     GCCCATCTAT   CTGT-AATTT   ATTGACGAAA   TAGACGAAAA   GGAAGGTGGC  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      GCCCAGCTAT   CTGTCACTTC   ATCAAAAGGA   CAGTAGAAAA   GGAAGGTGGC

101    TCCTATAAAG   CACATCATTG   CGATAACAGA   AAGGCCATTG   TTGAAGATAC  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      ACCTACAAAT   GCCATCATTG   CGATAAAGGA   AAGGCTATCG   TTCAAGATGC

151    CTCTGCTGAC   ATTGGTCCCC   AAGTGGAAGC   ACCACCCCAT   GAGGAGCACC  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      CTCTGCCGAC   AGTGGTCCCA   AAGATGGACC   CCCA-CCCAC   GAGGAGCATC

201    GTGGAGTAAG   AAGACGTTCG   AGCCACGTCG   AAAAAGCAAG   TGTGTTGATG  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      GTGGAAAAAG   AAGACGTTC   AACCACGTCT   TCAAAGCAAG   TGGATTGATG

251    TAGTATCTCC   ATTGACGTAA   GGGATGACGC   ACAATCCAAC   TATCCATCGC  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      TCATATCTCC   ACTGACGTAA   GGGATGACGC   ACAATCCCAC   TATCCTTCGC

301    AAGACCATTG   CTCTATATAA   GAAAGTTAAT   ATCATTTTGA   GTGGCCACGC  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      AAGACCCTTC   CTCTATATAA   GGAAGTTCAT   TTCATTTGGA   GAGGACACGC

351    TG                [SEQ ID NO:2]  
      | |  
      TG                [SEQ ID NO:3]

FIGURE 3

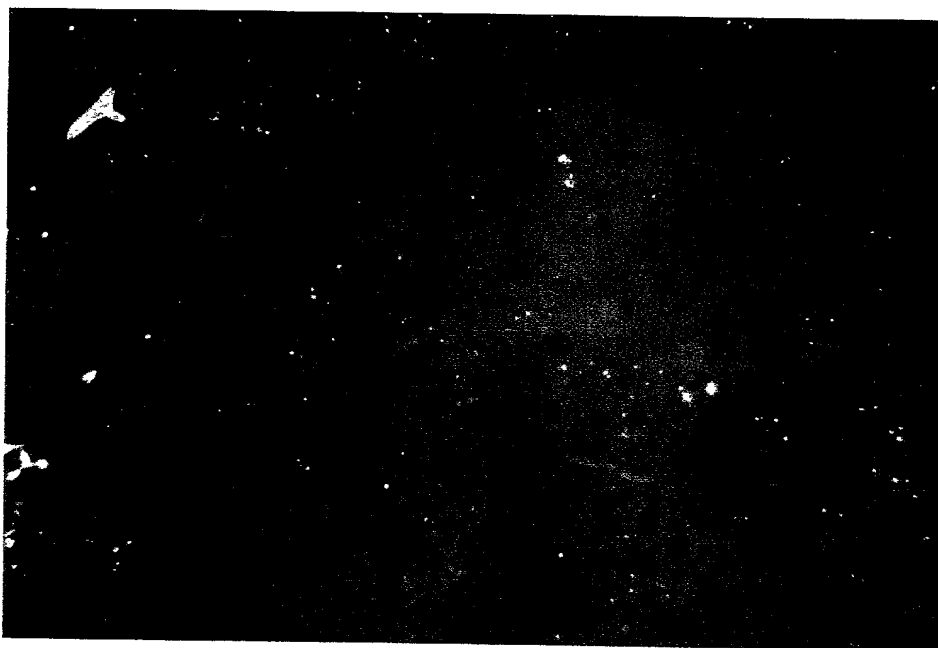


FIG. 4A

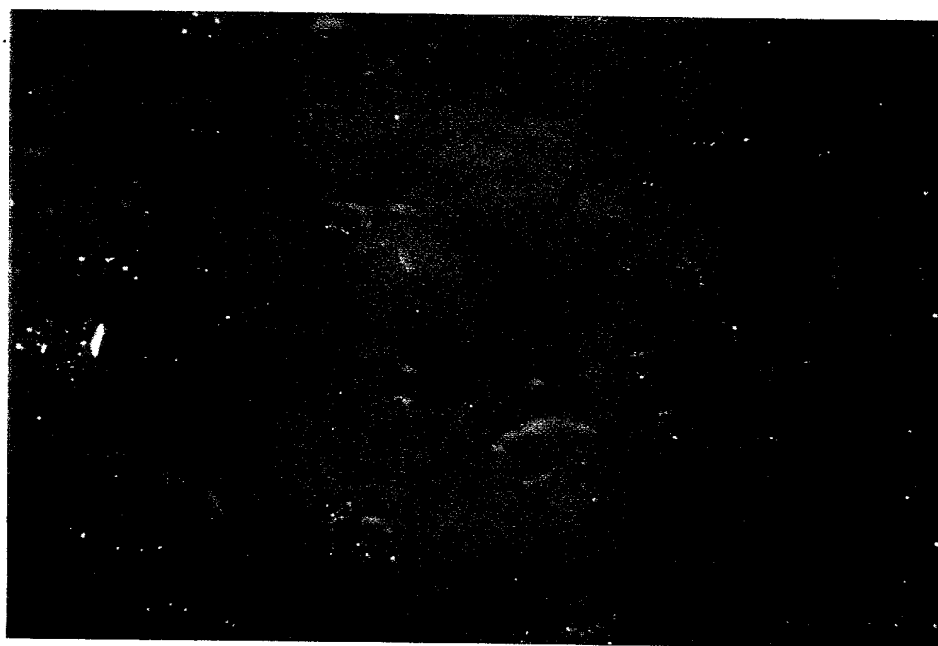


FIG. 4B